#### SEQUENCE LISTING

<110> Universiteit Utrecht Holding B.V.
<120> Piroplasmid vaccine
<130> 2003-010
<160> 20
<170> PatentIn version 3.2
<210> 1 <211> 1818 <212> DNA <213> Babesia bovis
<220> <221> CDS <222> (1)(1818)
<pre>&lt;400&gt; 1 atg cag tta cat aac aaa atg cag tca act tct ctc aaa tat aac tac</pre>
aag cgc atg ctt tgt atg gct ctt gta cca gtt atc tta tcg tca ttt  196 198 20 25 30
ttt gcg gaa gat gct tta gct tcc aac tcc acg ctt ttc gct ttc cac  Phe Ala Glu Asp Ala Leu Ala Ser Asn Ser Thr Leu Phe Ala Phe His  35  40  45
aag gaa cca aac aat cgt agg ctt acc aaa agg tct tca aga gga cag 192 Lys Glu Pro Asn Asn Arg Arg Leu Thr Lys Arg Ser Ser Arg Gly Gln 50 60
ttg ctc aac tca agg agg ggt tcg gat gcg tcc gaa tct tcc gat Leu Leu Asn Ser Arg Arg Gly Ser Asp Asp Ala Ser Glu Ser Ser Asp 70 75 80
aga tac cca ggt agg tcg ggt ggc tct aag aat tcg agc caa tcc ccc 288 Arg Tyr Pro Gly Arg Ser Gly Gly Ser Lys Asn Ser Ser Gln Ser Pro 85 90 95
tgg atc aag tat atg caa aag ttc gac att ccc cgt aac cac ggc tct Trp Ile Lys Tyr Met Gln Lys Phe Asp Ile Pro Arg Asn His Gly Ser 100 105 110
gga atc tat gtc gat ctt gga gga tat gaa tcc gtt ggt tca aaa agt 384 Gly Ile Tyr Val Asp Leu Gly Gly Tyr Glu Ser Val Gly Ser Lys Ser 115 120 125
tat cgt atg ccc gtt ggt aag tgc cca gta gtc ggt aaa att ata gac Tyr Arg Met Pro Val Gly Lys Cys Pro Val Val Gly Lys Ile Ile Asp 130 135 140
ctt gga aat ggt gcc gac ttc ctc gat ccc att tca tca gac gac cca Leu Gly Asn Gly Ala Asp Phe Leu Asp Pro Ile Ser Ser Asp Asp Pro

145	150	155	160
	Ala Phe Pro Glu	act gct gtg gac tct Thr Ala Val Asp Ser 170	
		tca tca gca tct gcg Ser Ser Ala Ser Ala 190	
		aga cgt tgg gga tat Arg Arg Trp Gly Tyr 205	
		gct agt aac ctc att Ala Ser Asn Leu Ile 220	_
		cct ttt gtt ttt gac Pro Phe Val Phe Asp 235	
	Ile Leu Tyr Ser	gcc ata caa tac aac Ala Ile Gln Tyr Asn 250	
		tcc gaa gat ggt aca Ser Glu Asp Gly Thr 270	
		gct gag gat gca cac Ala Glu Asp Ala His 285	
		tgg gaa gaa aat tgt Trp Glu Glu Asn Cys 300	
		aaa tgg tct ggt ggc Lys Trp Ser Gly Gly 315	
	Ala Phe Gln Glu	tat gcc aac agc act Tyr Ala Asn Ser Thr 330	
<del>_</del>	_	gca act gac ttg aat Ala Thr Asp Leu Asn 350	_
		aaa gaa ttg acc gat Lys Glu Leu Thr Asp 365	
		aac gct att ttt tct Asn Ala Ile Phe Ser 380	
		tca cgt ggt gtg ggt Ser Arg Gly Val Gly 395	

tgg gct aca t Trp Ala Thr 1	_	_		_	_	1248
aca cct aac t Thr Pro Asn C	-		a Gly Ser	_		1296
ata ggt tca c Ile Gly Ser I 435						1344
gac acc aat o Asp Thr Asn 0 450						1392
ctt gat gtt c Leu Asp Val I 465						1440
aaa tgc gat g Lys Cys Asp A			_			1488
tat ttc ctt t Tyr Phe Leu C			o Asn Trp			1536
cac atg atc of His Met Ile 0 515				_	~ ~ ~	1584
tgt acc act a Cys Thr Thr 1 530						1632
atc aag gct a Ile Lys Ala I 545			_	•		1680
agc aac tat g Ser Asn Tyr A						1728
cag cgt ttg g Gln Arg Leu <i>I</i>			r Trp Gly			1776
cca agt gat g Pro Ser Asp V 595						1818

<sup>&</sup>lt;210> 2 <211> 605 <212> PRT <213> Babesia bovis

<sup>&</sup>lt;400> 2

Met Gln Leu His Asn Lys Met Gln Ser Thr Ser Leu Lys Tyr Asn Tyr 1 5 10 15

Lys Arg Met Leu Cys Met Ala Leu Val Pro Val Ile Leu Ser Ser Phe 20 25 30

Phe Ala Glu Asp Ala Leu Ala Ser Asn Ser Thr Leu Phe Ala Phe His

35 40 45

Lys Glu Pro Asn Asn Arg Arg Leu Thr Lys Arg Ser Ser Arg Gly Gln 50 55 60

Leu Leu Asn Ser Arg Arg Gly Ser Asp Asp Ala Ser Glu Ser Ser Asp 65 70 75 80

Arg Tyr Pro Gly Arg Ser Gly Gly Ser Lys Asn Ser Ser Gln Ser Pro

Trp Ile Lys Tyr Met Gln Lys Phe Asp Ile Pro Arg Asn His Gly Ser 100 105 110

Gly Ile Tyr Val Asp Leu Gly Gly Tyr Glu Ser Val Gly Ser Lys Ser 115 120 125

Tyr Arg Met Pro Val Gly Lys Cys Pro Val Val Gly Lys Ile Ile Asp 130 135 140

Leu Gly Asn Gly Ala Asp Phe Leu Asp Pro Ile Ser Ser Asp Asp Pro 145 . 150 . 155 . 160

Ser Tyr Arg Gly Leu Ala Phe Pro Glu Thr Ala Val Asp Ser Asn Ile 165 170 175

Pro Thr Gln Pro Lys Thr Arg Gly Ser Ser Ser Ala Ser Ala Ala Lys
180 185 190

Leu Ser Pro Val Ser Ala Lys Asp Leu Arg Arg Trp Gly Tyr Glu Gly
195 200 205

Asn Asp Val Ala Asn Cys Ser Glu Tyr Ala Ser Asn Leu Ile Pro Ala 210 215 220

Ser Asp Arg Ser Thr Lys Tyr Arg Tyr Pro Phe Val Phe Asp Ser Asp 225 230 235

Asn Gln Met Cys Tyr Ile Leu Tyr Ser Ala Ile Gln Tyr Asn Gln Gly 245 250 255

Asn Arg Tyr Cys Asp Asn Asp Gly Ser Ser Glu Asp Gly Thr Ser Ser 260 265 270

Leu Leu Cys Met Lys Pro Tyr Lys Ser Ala Glu Asp Ala His Leu Tyr 275 280 285

Tyr Gly Ser Ala Lys Val Asp Pro Asp Trp Glu Glu Asn Cys Pro Met 290 295 300

His Pro Val Arg Asp Ala Ile Phe Gly Lys Trp Ser Gly Gly Ser Cys 305 310 315 320

Val Ala Ile Ala Pro Ala Phe Gln Glu Tyr Ala Asn Ser Thr Glu Asp 325 330 335

Cys Ala Ala Ile Leu Phe Asp Asn Ser Ala Thr Asp Leu Asn Ile Glu 340 345 350

Ala Val Asn Glu Asp Phe Asn Glu Leu Lys Glu Leu Thr Asp Gly Leu 355 360 365

Lys Arg Leu Asn Met Ser Lys Val Ala Asn Ala Ile Phe Ser Pro Leu 370 375 380

Ser Asn Val Ala Gly Thr Ser Arg Ile Ser Arg Gly Val Gly Met Asn 385 390 395 400

Trp Ala Thr Tyr Asp Lys Asp Ser Gly Met Cys Ala Leu Ile Asn Glu 405 410 415

Thr Pro Asn Cys Leu Ile Leu Asn Ala Gly Ser Ile Ala Leu Thr Ala 420 425 430

Ile Gly Ser Pro Leu Glu Tyr Asp Ala Val Asn Tyr Pro Cys His Ile 435 440 445

Asp Thr Asn Gly Tyr Val Glu Pro Arg Ala Lys Asn Thr Asn Lys Tyr 450 460

Leu Asp Val Pro Phe Glu Val Thr Thr Ala Leu Ser Met Lys Thr Leu 465 470 475 480

Lys Cys Asp Ala Tyr Val His Thr Lys Tyr Ser Asp Ser Cys Gly Thr

6/29

485 490 495 Tyr Phe Leu Cys Ser Asp Val Lys Pro Asn Trp Phe Ile Arg Phe Leu 500 505 His Met Ile Gly Leu Tyr Asn Thr Lys Arg Ile Val Ile Phe Val Cys 520 515 Cys Thr Thr Thr Ala Ile Val Leu Thr Ile Trp Ile Trp Lys Arg Phe 530 535 Ile Lys Ala Lys Lys Glu Pro Ala Pro Pro Ser Phe Asp Lys Tyr Leu 545 550 560 Ser Asn Tyr Asp Tyr Asp Thr Thr Leu Asp Ala Asp Asn Glu Thr Glu Gln Arg Leu Asp Ser Ser Ala Tyr Ser Trp Gly Glu Ala Val Gln Arg 580 585 Pro Ser Asp Val Thr Pro Val Lys Leu Ser Lys Ile Asn 595 600 <210> 3 <211> 2349 <212> DNA <213> Theileria annulata <220> <221> CDS <222> (1)..(2349) atg aaa aaa ata gga ctt aaa att agg gca caa aag gat aaa tta aat Met Lys Lys Ile Gly Leu Lys Ile Arg Ala Gln Lys Asp Lys Leu Asn 48 cct gtg tta gga agc aac tct gac cct tcg gaa gag tat gat tca ttc 96 Pro Val Leu Gly Ser Asn Ser Asp Pro Ser Glu Glu Tyr Asp Ser Phe cag caa aat gtt ttc act cat caa cca acc caa cta cac aaa tct cat 144 Gln Gln Asn Val Phe Thr His Gln Pro Thr Gln Leu His Lys Ser His 40 cac tac att aca cac cag aaa aaa acc agc caa cac atc gac gat tta 192 His Tyr Ile Thr His Gln Lys Lys Thr Ser Gln His Ile Asp Asp Leu 55 aat ttt tat aat gga aaa ttt aat caa aag agc aga att ggt cca ggg 240 Asn Phe Tyr Asn Gly Lys Phe Asn Gln Lys Ser Arg Ile Gly Pro Gly

65	70	75	80
		g gta gaa ggt gaa aca 1 Val Glu Gly Glu Thr 90	
		a ata aag tca aaa aca s Ile Lys Ser Lys Thr 5 110	
		a tca ttt tta gct gtt 1 Ser Phe Leu Ala Val 125	
	_	a gag gaa cct ttt act 1 Glu Glu Pro Phe Thr 140	
		a tca tta att caa agc l Ser Leu Ile Gln Ser 155	
		a act caa aat tca agt r Thr Gln Asn Ser Ser 170	
		t aat acc tca tta ata n Asn Thr Ser Leu Ile 5 190	
		a ggt aga ttc gga tca 1 Gly Arg Phe Gly Ser 205	
caa tca gga ttg ata Gln Ser Gly Leu Ile 210	agc agt aga gc Ser Ser Arg Ala 215	a gac aaa aag aag cgg a Asp Lys Lys Arg 220	tct ggt 672 Ser Gly
		g aaa ggg aag gga gga s Lys Gly Lys Gly Gly 235	
		t ttc atg gca aag ttt p Phe Met Ala Lys Phe 250	
		c gta gat ttg ggt gaa r Val Asp Leu Gly Glu 5 270	
		g cct ata gga aaa tgt t Pro Ile Gly Lys Cys 285	
		t gga gct gat ttt ttg n Gly Ala Asp Phe Leu 300	
		a ggg ctg ggg ttc cct g Gly Leu Gly Phe Pro 315	

aaa gtt Lys Val															1008
tca cca Ser Pro		_	_	_	_			_						_	1056
tca gat Ser Asp															1104
agt aat Ser Asr 370	Arg			_		_		_		-		_			1152
gag aag Glu Lys 385															1200
gta aag Val Lys		_	_		_		_	_	_			_	_		1248
gct tgt Ala Cys															1296
gga acc Gly Thi															1344
cct att Pro Ile 450	Arg	-	_						_	-			_	_	1392
tgt gtt Cys Val 465															1440
gca tgt Ala Cys															1488
agc aca Ser Thi															1536
atg aat Met Asr			_	_	_		_				-		-		1584
agg tad Arg Ty: 530	Ser														1632
tgg gct Trp Ala 545															1680

gtt Val	ccc Pro	agc Ser	tgt Cys	ctt Leu 565	att Ile	ata Ile	agt Ser	aac Asn	ggc Gly 570	cac His	tat Tyr	gcc Ala	ctt Leu	aca Thr 575	agt Ser	1728
ctc Leu	agc Ser	tca Ser	ccc Pro 580	aat Asn	gaa Glu	gag Glu	gat Asp	gct Ala 585	ata Ile	aat Asn	tac Tyr	ccc Pro	tgc Cys 590	gat Asp	atc Ile	1776
	cag Gln															1824
	cag Gln 610															1872
ggt Gly 625	gct Ala	gaa Glu	aac Asn	aaa Lys	ccc Pro 630	aaa Lys	gag Glu	aaa Lys	ggt Gly	aaa Lys 635	tct Ser	gag Glu	aaa Lys	aag Lys	aat Asn 640	1920
	aaa Lys															1968
	gag Glu															2016
	tgc Cys															2064
	aag Lys 690															2112
Val 705	ctg Leu	Ala	Val	Leu	Ala 710	Tyr	Phe	Gly	Tyr	Arg 715	Tyr	Tyr	Ser	Lys	Asn 720	2160
	ttg Leu															2208
aac Asn	tac Tyr	tac Tyr	aat Asn 740	gag Glu	gac Asp	ttt Phe	gat Asp	gac Asp 745	gaa Glu	caa Gln	gat Asp	cgg Arg	gat Asp 750	gaa Glu	tac Tyr	2256
	tcg Ser															2304
	tct Ser 770													taa		2349

<sup>&</sup>lt;210> 4 <211> 782 <212> PRT <213> Theileria annulata

PCT/EP2004/052169

<400> 4

Met Lys Lys Ile Gly Leu Lys Ile Arg Ala Gln Lys Asp Lys Leu Asn

Pro Val Leu Gly Ser Asn Ser Asp Pro Ser Glu Glu Tyr Asp Ser Phe 25 30

Gln Gln Asn Val Phe Thr His Gln Pro Thr Gln Leu His Lys Ser His 40

His Tyr Ile Thr His Gln Lys Lys Thr Ser Gln His Ile Asp Asp Leu 55

Asn Phe Tyr Asn Gly Lys Phe Asn Gln Lys Ser Arg Ile Gly Pro Gly 70 75

Lys Val Val Asn Asn Ser Arg Asn Leu Val Glu Gly Glu Thr Leu Ser 85

Lys Asp Asp Asn Lys Thr Lys Ser Lys Ile Lys Ser Lys Thr Ala Ser

Ile Leu Pro Arg Leu Leu Lys Ser Leu Ser Phe Leu Ala Val Leu Gly

Ser Ile Asn Ser Phe Ser Leu Ala Leu Glu Glu Pro Phe Thr Gln His 130

Thr Ser Asn Arg Thr Pro Phe Glu Val Ser Leu Ile Gln Ser Asn Ser

Ser Leu Ser Pro Ile His Asn Ser Ser Thr Gln Asn Ser Ser His His 170 165

Asn Gly Phe Ser Gly Ser Thr Val Asn Asn Thr Ser Leu Ile Glu Thr

Arg Asn Asn Val Leu Asn Arg Thr Leu Gly Arg Phe Gly Ser Phe Leu 200 205

Gln Ser Gly Leu Ile Ser Ser Arg Ala Asp Lys Lys Lys Arg Ser Gly

Met Asn Arg Arg Gly Pro Lys Gly Lys Gly Lys Gly Gly Glu Asp

225
230
235
240

Glu Glu Lys Arg Asn Lys Trp Thr Asp Phe Met Ala Lys Phe Asp Ile 255

Ala Lys Val His Gly Ser Gly Val Tyr Val Asp Leu Gly Glu Ser Ala 260

Thr Val Gly Ser Tyr Asp Tyr Arg Met Pro Ile Gly Lys Cys Pro Val 285

Val Gly Lys Ala Ile Ile Leu Glu Asn Gly Ala Asp Phe Leu Ser Ser 290 295 300

Ile Thr His His Asp Pro Lys Glu Arg Gly Leu Gly Phe Pro Ala Thr 305 310 315 320

Lys Val Ala Ser Asn Ser Ser Lys Leu Asp Met Glu Asn Gln Leu Leu 325 330 335

Ser Pro Ile Ser Ala Gln Val Leu Arg Ser Trp Asn Tyr Lys His Glu 340 345 350

Ser Asp Leu Ser Asn Cys Ala Glu Tyr Ser Arg Asn Ile Val Pro Gly 355 360 365

Ser Asn Arg Asn Ser Lys Tyr Arg Tyr Pro Phe Val Tyr Asp Glu Ser 370 380

Glu Lys Leu Cys Tyr Ile Leu Tyr Ser Pro Met Gln Tyr Asn Gln Gly 385 390 395 400

Val Lys Tyr Cys Asp Gln Asp Ser Pro Asp Glu Gly Thr Ser Ser Leu 405 410 415

Ala Cys Met Tyr Pro Asp Lys Ser Lys Glu Asp Ser His Leu Phe Tyr 420 425 430

Gly Thr Ser Gly Leu His Met Asp Trp Pro Val Val Cys Pro Val Tyr 435 440 445

Pro Ile Arg Asp Ser Ile Phe Gly Ser Tyr Asp Asp Gln Lys Asp Glu 450 455 460

Cys Val Pro Ile Glu Pro Ile Phe Glu Glu Glu Ala Glu Asp Tyr Glu 465 470 475 480

#### WO 2005/026199 PCT/EP2004/052169 12/29

Ala Cys Ala	Lys Ile 485	Ile Ph	e Glu	Tyr	Ser 490	Pro	Ser	Asp	Val	Asp 495	Ile
Ser Thr Asn	Asn Gln 500	Lys Le	u Ser	Asp 505	Val	Asp	Leu	Tyr	Lys 510	Glu	Ala
Met Asn Asn 515	Gly Lys	Leu Se	r Thr 520	Ala	Leu	Ser	Ile	Met 525	Phe	Ala	Pro
Arg Tyr Ser 530	Glu Asp	Arg Pr 53		Tyr	Thr	Lys	Gly 540	Val	Gly	Ile	Asn
Trp Ala Thr 545	Tyr Ser	Val G] 550	u Glu	Lys	Lys	Cys 555	Asn	Ile	Leu	Asp	Val 560
Val Pro Ser	Cys Leu 565	Ile Il	e Ser	Asn	Gly 570	His	Tyr	Ala	Leu	Thr 575	Ser
Leu Ser Ser	Pro Asn 580	Glu Gl	u Asp	Ala 585	Ile	Asn	Tyr	Pro	Cys 590	Asp	Ile
Val Gln Gly 595	Lys Gly	Phe Le	u Lys 600	Asn	Pro	Asn	Gly	Gly 605	Lys	Lys	Asn
Ala Gln Glu 610	Pro Pro	Lys Gl		Glu	Pro	Glu	Glu 620	Pro	Lys	Lys	Glu
Gly Ala Glu 625	Asn Lys	Pro Ly 630	s Glu	Lys	Gly	Lys 635	Ser	Glu	Lys	Lys	Asn 640
Glu Lys Ser	Met Pro 645	Ser G	y Pro	Phe	Thr 650	Pro	Tyr	Thr	Ser	Leu 655	ГЛа
Lys Glu Gly	Phe Glu 660	Cys Se	r Lys	Tyr 665	Thr	Val	Glu	Arg	Val 670	Asn	Lys
Ser Cys Gly 675	_	Tyr G	u Cys 680		Glu	Thr	Pro	Val 685	Leu	Phe	Thr
Lys Lys Asn 690	Arg Ile	Tyr Le	_	Ile	Ile	Leu	Ala 700	Val	Ser	Leu	Val
Val Leu Ala 705	Val Leu	Ala Ty 710	r Phe	Gly	Tyr	Arg 715	туг	Tyr	Ser	Lys	Asn 720

#### WO 2005/026199 PCT/EP2004/052169 13/29

His Leu Lys Lys Hi. 72		Ile Tyr Glu Asp 730	Asp Asn Val Asn 735	
Asn Tyr Tyr Asn Gl	a Asp Phe Asp	Asp Glu Gln Asp 745	Arg Asp Glu Tyr 750	
Ala Ser Asn Val Ar 755	G Gly Asp Gln 760	_	His Thr Pro Asp 765	
Arg Ser Glu Val Th 770	r Pro Val Arg 775	Ile Ser Arg Leu 780	Asn His	
<210> 5 <211> 1968 <212> DNA <213> Babesia bov	is			
<220> <221> CDS <222> (1)(1968)				
<pre>&lt;400&gt; 5 atg atc ggt tac at Met Ile Gly Tyr Il 1 5</pre>				48
gcc ttt tta gct ac Ala Phe Leu Ala Th 20				96
ggt tca cca aag gg Gly Ser Pro Lys Gl 35				144
gtg gta gat gaa tc Val Val Asp Glu Se 50				192
atg att cca ttt tt Met Ile Pro Phe Le 65				240
act gac ata cgt ct Thr Asp Ile Arg Le 85	_			288
ata ttt acg ttt tt Ile Phe Thr Phe Le 100			22 2	336
acg aaa ctt gat tg Thr Lys Leu Asp Tr 115				384

## WO 2005/026199 PCT/EP2004/052169 14/29

Tyr					ctg Leu											432
ggt Gly 145																480
					tac Tyr											528
_		_		_	atg Met	_			_		_	_		_	_	576
gaa Glu	_	_			gta Val		_	_			_	_	_		_	624
					tgg Trp	-								_		672
_			_	_	gat Asp 230				_	_	_	_	_			720
					tca Ser											768
	_		_	_	ctt Leu	_	_		_	_		_	_		_	816
					caa Gln											864
					tca Ser			_			_	_				912
	-		_	_	ccg Pro 310	_		_		_	_	_	-			960
_				_	aca Thr	_	_		_	_	_					1008
					tcc Ser											1056
_			_		act Thr	_	_			_			_	_		1104
tca	agc	cct	act	gac	atg	tca	tca	agt	cac	agt	gac	atg	cca	tca	act	1152

							_	13/27								
Ser	Ser 370	Pro	Thr	Asp	Met	Ser 375	Ser	Ser	His	Ser	Asp 380	Met	Pro	Ser	Thr	
					tca Ser 390											1200
					cac His											1248
					gat Asp											1296
					atg Met											1344
		_		_	aat Asn							_				1392
					gat Asp 470											1440
					cgc Arg											1488
		_	_	_	ctt Leu	_	_	_	_	_		_	_			1536
					tat Tyr											1584
					gta Val											1632
cac His 545	gag Glu	gtg Val	tat Tyr	gac Asp	gat Asp 550	cac His	ccc Pro	gag Glu	gaa Glu	tct Ser 555	gaa Glu	aac Asn	acc Thr	gjà aaa	att Ile 560	1680
					gaa Glu											1728
					cgt Arg									Ala		1776
ggt Gly	gct Ala	cta Leu 595	cta Leu	ggt Gly	ctt Leu	ctt Leu	ctc Leu 600	ctt Leu	ggt Gly	gcc Ala	ggt Gly	ggt Gly 605	gga Gly	tac Tyr	gct Ala	1824

atg tac aaa aag aac aag aca cct act gtt gag aca ggt tca ggt gat Met Tyr Lys Lys Asn Lys Thr Pro Thr Val Glu Thr Gly Ser Gly Asp 1872

1920

1968

610 615 620 tac act ggg gcc gac gag agt tca gaa ccc atg aag gag ggt gac aca Tyr Thr Gly Ala Asp Glu Ser Ser Glu Pro Met Lys Glu Gly Asp Thr 625 630 635 tac acc gtc act gag ttt gac aac att tgg ggc gag gca gcg taa Tyr Thr Val Thr Glu Phe Asp Asn Asn Ile Trp Gly Glu Ala Ala <210> 6 <211> 655 <212> PRT <213> Babesia bovis <400> 6 Met Ile Gly Tyr Ile Lys Ile Leu Ala Ser Val Pro Leu Leu Ser Leu Ala Phe Leu Ala Thr Thr Gly Ile His Ala Phe Ala Asp Lys Gly Ile Gly Ser Pro Lys Gly Lys Gln Cys Lys Lys Gln Leu Asp Phe Ser Ile 35 40 Val Val Asp Glu Ser Ala Ser Ile Ser Asp Asp Gln Trp Glu Gly Gln 50 Met Ile Pro Phe Leu Arg Asn Leu Ile His Thr Val Asp Leu Asp Asn 70 Thr Asp Ile Arg Leu Ser Leu Thr Thr Tyr Ser Thr Pro Thr Arg Gln 85 Ile Phe Thr Phe Leu Asp Ala Ala Ser Ser Thr Arg Leu Ala Leu 100 105 Thr Lys Leu Asp Trp Met Asn Gly Thr Lys Ala Arg Tyr Gly Met Thr 120 Tyr Thr Gly Arg Ala Leu Asn Tyr Val Arg Lys Ala Ile Leu Pro Tyr 135 Gly Arg Lys Asn Val Pro Lys Ala Leu Leu Leu Ile Thr Asp Gly Val

Ser Ser Asp Gly Ser Tyr Thr Ala Gln Val Ala Ala Met Leu Arg Asp

Glu Gly Val Asn Val Met Val Ile Gly Val Gly Asp Val Asn Val Ala 180 185 190

Glu Cys Arg Gly Ile Val Gly Cys Asp Gly Ile Met Asp Cys Pro Met 195 200 205

Phe Lys Gln Thr Asn Trp Lys Asp Ile Met Gly Leu Phe Asn Ser Leu 210 215 220

Met Lys Glu Val Cys Asp Ile Leu Pro Gln Asp Ala Val Cys Glu Pro 225 230 235 240

Val Trp Ala Glu Trp Ser Ser Cys Asn Gly Glu Cys Gly Val Pro Gly 245 250 255

Lys Arg Thr Arg Ala Leu Leu Asp Leu Arg Met Ile Glu Lys Pro Val 260 265 270

Asn Gly Ser Asn Gly Gln Pro Gly Lys Ser Cys Glu Asp Gln Lys Met 275 280 285

Asn Phe Leu Pro Gln Ser Glu Thr Cys Thr Ile Glu Cys Asn His Glu 290 295 300

Pro Val Pro Ser Ser Pro Glu Pro Val Ser Asp Asp Met Asp His Pro 305 310 315 320

Glu Pro Thr Pro Val Thr Pro Glu Gly Asp Met Asp Lys Ser His Ser 325 330 335

His Ser Ser Ile Pro Ser Thr Pro Asp Met Pro Ser Ser His Ser Asp 340 345 350

Met Ser Ser Ser Pro Thr Asp Met Ser Ser Ser Pro Thr Asp Met Ser 355 360 365

Ser Ser Pro Thr Asp Met Ser Ser Ser His Ser Asp Met Pro Ser Thr 370 375 380

Pro Thr Gly Met Ser Ser His Ser Asp Met Pro Ser Ser His Ser 385 390 395 400

Asp Met Pro Ser Ser His Ser Asp Met Ser Ser Ser Pro Thr Asp Met 405 410 415

Ser Ser Ser His Ala Asp Thr Arg Val Gly Asn Thr Asp Glu Glu His Asn His Arg Lys Asp Met Asp Val Lys Phe Pro Glu Asn Met Asp Asp Ile Pro Val Glu Asp Asn Pro Ile Pro Thr Asp Pro Arg His Gly Val 455 Glu Pro Ser Pro Ser Asp Val Ile Pro Glu Asp Asp Gln Leu Arg Arg 465 470 475 Thr Leu Glu Met Gln Arg Glu Glu Asp Leu Lys Lys Glu Leu Met Leu Gln His Glu Leu Lys Leu Gln Glu Glu Lys Glu Arg Ala Ala Ile Leu Glu Asn Asn Thr Pro Tyr Gly Ser Ala Thr Ser Val Ser Gln Asp Gly Glu Ser Pro Thr Gly Val Pro Gln Ser Ser Glu Thr Asp Ala Ile Arg His Glu Val Tyr Asp Asp His Pro Glu Glu Ser Glu Asn Thr Gly Ile Asn Ala Asp Val Thr Glu Ser Glu Asp Tyr Glu Gly Glu Lys Gln Lys Asp Glu Ser Asn Glu Arg Ser Thr Ser Asn Thr Thr Lys Ile Ala Gly 580 Gly Ala Leu Leu Gly Leu Leu Leu Gly Ala Gly Gly Tyr Ala 595 Met Tyr Lys Lys Asn Lys Thr Pro Thr Val Glu Thr Gly Ser Gly Asp 610 615 Tyr Thr Gly Ala Asp Glu Ser Ser Glu Pro Met Lys Glu Gly Asp Thr

Tyr Thr Val Thr Glu Phe Asp Asn Asn Ile Trp Gly Glu Ala Ala 645 650 655

<210> 7 <211> 1047 <212> DNA <213> Theileria annulata

<220>

<221> CDS

<222> (1)..(1047) gat aag ggg cta tat cct gac ggt ata aag aaa ccg agc tcc tac tgc 48 Asp Lys Gly Leu Tyr Pro Asp Gly Ile Lys Lys Pro Ser Ser Tyr Cys 10 cac agg gaa ttg gac tta aca ata tta gtc gat gaa tcc tcg agt atc 96 His Arg Glu Leu Asp Leu Thr Ile Leu Val Asp Glu Ser Ser Ile tat att gaa gag tgg aac aaa ctc att cca ttt ctt aaa tca ctg gtg 144 Tyr Ile Glu Glu Trp Asn Lys Leu Ile Pro Phe Leu Lys Ser Leu Val 35 aga tca ata aat ata agt cca aat tat gtg cac ttg tca atg gtc acc 192 Arg Ser Ile Asn Ile Ser Pro Asn Tyr Val His Leu Ser Met Val Thr ttt tcc act tca att cgg tgg tta ata tca ttt ctc gac cca gcc tct 240 Phe Ser Thr Ser Ile Arg Trp Leu Ile Ser Phe Leu Asp Pro Ala Ser aag gat gag caa ttg gcc ctt gct gtt ctg gac aag ctg aag aac agt 288 Lys Asp Glu Gln Leu Ala Leu Ala Val Leu Asp Lys Leu Lys Asn Ser aag oot gtg ttt ggg tac aca ttc act gga cag gca ctt aac ttt att 336 Lys Pro Val Phe Gly Tyr Thr Phe Thr Gly Gln Ala Leu Asn Phe Ile tct gag gct gtt tat atg ttt ggt gct agg cgt aac tct cca aag ggc 384 Ser Glu Ala Val Tyr Met Phe Gly Ala Arg Arg Asn Ser Pro Lys Gly 120 125

atc att atc acc gac gga tcc tct act cag aca aac gtt act tct 432 Ile Ile Ile Ile Thr Asp Gly Ser Ser Thr Gln Thr Asn Val Thr Ser 135

cag gcg tcg gct cta cta agg gat gct ggt gta aca att cta gtt gtt 480 Gln Ala Ser Ala Leu Leu Arg Asp Ala Gly Val Thr Ile Leu Val Val 150 155

gga gtt ggg aag gct aaa gaa agc gag tgt aga ggt ata gtt ggt tgt 528 Gly Val Gly Lys Ala Lys Glu Ser Glu Cys Arg Gly Ile Val Gly Cys

tct acc aaa gga gag tgc ccc ctt ttc ttt atg acc aac tgg gat gaa 576 Ser Thr Lys Gly Glu Cys Pro Leu Phe Phe Met Thr Asn Trp Asp Glu

att atc agg aag gtt ggg gag ttg atg gct gag gtt tgt gag acc att 624 Ile Ile Arg Lys Val Gly Glu Leu Met Ala Glu Val Cys Glu Thr Ile

20/29

195	20	00	205	
cct aag gac gcc g Pro Lys Asp Ala v 210		ro Ile Trp Ser		
gac gcc aag tgc ( Asp Ala Lys Cys ( 225				_
act aca att tct of the state of				
aca tgt gag atg a Thr Cys Glu Met 1 260				
tcc gtt gag tct a Ser Val Glu Ser : 275	Lys Ile Ala G			_
ctt gca ggc gga g Leu Ala Gly Gly ( 290		hr Tyr Tyr Lys l		
aga gtg agt gaa Arg Val Ser Glu 305				
ggg aac cgt ggt Gly Asn Arg Gly				
gat tta gat gat Asp Leu Asp Asp 340				1047
<210> 8 <211> 348 <212> PRT <213> Theileria	annulata			
<400> 8				
Asp Lys Gly Leu 1	Tyr Pro Asp G 5	ly Ile Lys Lys 1 10	Pro Ser Ser Tyr 15	Cys
His Arg Glu Leu 20	Asp Leu Thr I	le Leu Val Asp ( 25	Glu Ser Ser Ser 30	Ile

Arg Ser Ile Asn Ile Ser Pro Asn Tyr Val His Leu Ser Met Val Thr

Tyr Ile Glu Glu Trp Asn Lys Leu Ile Pro Phe Leu Lys Ser Leu Val

Phe Ser Thr Ser Ile Arg Trp Leu Ile Ser Phe Leu Asp Pro Ala Ser 70 Lys Asp Glu Gln Leu Ala Leu Ala Val Leu Asp Lys Leu Lys Asn Ser Lys Pro Val Phe Gly Tyr Thr Phe Thr Gly Gln Ala Leu Asn Phe Ile Ser Glu Ala Val Tyr Met Phe Gly Ala Arg Arg Asn Ser Pro Lys Gly 120 115 Ile Ile Ile Thr Asp Gly Ser Ser Thr Gln Thr Asn Val Thr Ser Gln Ala Ser Ala Leu Leu Arg Asp Ala Gly Val Thr Ile Leu Val Val 145 150 155 Gly Val Gly Lys Ala Lys Glu Ser Glu Cys Arg Gly Ile Val Gly Cys Ser Thr Lys Gly Glu Cys Pro Leu Phe Phe Met Thr Asn Trp Asp Glu Ile Ile Arg Lys Val Gly Glu Leu Met Ala Glu Val Cys Glu Thr Ile Pro Lys Asp Ala Val Cys Lys Pro Ile Trp Ser Asp Trp Ser Lys Cys 210 215 220 Asp Ala Lys Cys Gly Ile Gly Thr Arg Tyr Gln Lys Leu Met Gly Val 225 Thr Thr Ile Ser Glu Pro Thr Val Gly Thr Asn Gly Lys Ser Gly Arg

Thr Cys Glu Met Ile Tyr Glu Asn Val Glu Val Pro Lys Glu Glu Cys 260

Ser Val Glu Ser Lys Ile Ala Gly Gly Val Ala Leu Ala Leu Leu Met

Leu Ala Gly Gly Gly Tyr Thr Tyr Tyr Lys Lys Tyr Gly Leu Ser 290 295 300

#### WO 2005/026199 PCT/EP2004/052169

Arg Val Ser Glu Thr Thr Asn Leu Asp Glu Asp Phe Ala Asp Ser Ser 310 315 Gly Asn Arg Gly Val Arg Glu Ser Val Gly Glu Ala Tyr Thr Val Thr 325 330 Asp Leu Asp Asp Gly Leu Trp Ser Gln Ser Asn Gln <210> 9 <211> 2259 <212> DNA <213> Babesia bovis <220> <221> CDS <222> (552)..(2189) <400> 9 ataagatgta gcactgatgt gtgtactcgg actctgacac tggagtatag gctaccagaa 60 ctgggcgcaa ctccctaatg gagtgccgct cccaggaggc cacagaacaa tggagtacaa 120 cgctcaaaac cgcagtgaat gttagctaca atatgtacat attgtcatgg agttcgtaat 180 cctaacaaag gccattgtat cgtcaatgtg gtctaccagt ggacgtcgct tgtggaggcc 240 agggtacatc aaatccctga gaacacctat cgtccggtgt tacggtggta atgggttact 300 ataaaagcaa atttaattgt agatattgta aaaaaactgt aaaattggtt agtgcttgca 360 ccgtcctggt cccgcgattt ggataccgct gtgctacgct ttgcacggaa tcacqacqtc 420 gtgcataacg ctgtgcttat gacttcgtac acatcaaacg actttaactg ccgttggttt 480 atatacgttg gcgttaggtt gttttgggtg ttattgtact gtggaatcat acacattcta 540 cacgtgtcat g atg gtg aag ttc cac aca tta tcg gtt gca gcc atc ctg 590 Met Val Lys Phe His Thr Leu Ser Val Ala Ala Ile Leu gcg att gct tca tcc aat act att ttt gct aca ttt aga tca aat gga 638 Ala Ile Ala Ser Ser Asn Thr Ile Phe Ala Thr Phe Arg Ser Asn Gly 20 aaa acc ttc gga gat gaa tct gtt agc ctt cta gaa cat gaa agt acc 686 Lys Thr Phe Gly Asp Glu Ser Val Ser Leu Leu Glu His Glu Ser Thr 35 40 agt ttg tct cgt ggt cct aga cca acc gaa gat caa atc agt cag tta 734 Ser Leu Ser Arg Gly Pro Arg Pro Thr Glu Asp Gln Ile Ser Gln Leu 50

cca aaa aat gtt ttc ttt cta ttg gat aac agc att gat atg tct att

Pro Lys Asn Val Phe Phe Leu Leu Asp Asn Ser Ile Asp Met Ser Ile
65 70 75

782

# WO 2005/026199 PCT/EP2004/052169 23/29

					aat Asn											830
					gga Gly											878
					tcg Ser 115											926
					att Ile											974
_					gga Gly	_	_			_				_		1022
	_			_	ttc Phe		_							_	_	1070
				_	ggt Gly	_	_		_	_						1118
					cca Pro 195											1166
					aga Arg											1214
					cag Gln		_		_					_	_	1262
_				_	aaa Lys									-	_	1310
_					gtg Val			_			_		_	_	_	1358
					tat Tyr 275											1406
	_			_	ttg Leu										_	1454
		_			atc Ile					_	_		_		_	1502
gat	atg	cag	aaa	aga	caa	ata	ttt	tgc	tac	tca	aat	aag	tgt	gct	ccc	1550

Asp	Met	Gln 320	Lys	Arg	Gln	Ile	Phe 325	Cys	Tyr	Ser	Asn	Lys 330	Cys	Ala	Pro	
					tct Ser											1598
					gag Glu 355											1646
					gag Glu											1694
gaa Glu	acg Thr	ctt Leu	tct Ser 385	gga Gly	agc Ser	gcc Ala	cgt Arg	gta Val 390	gaa Glu	aca Thr	agc Ser	tta Leu	gaa Glu 395	.agc Ser	tca Ser	1742
					gtg Val											1790
					tac Tyr											1838
					gtt Val 435											1886
	_	-	-	_	cag Gln		_	_	-							1934
					cca Pro											1982
					atc Ile											2030
_	-			_	ggc Gly	-						_				2078
					gaa Glu 515											2126
					ctc Leu											2174
	aca Thr		_	taa	gaca	acga	aac g	gggtl	igte	ac ag	gccaa	acata	a ta	caaat	tgca	2229
gtt	gtttaaatta agtcactagt taaaaaaaaa											2259				

<210> 10

<211> 545 <212> PRT <213> Babesia bovis

<220>

<221> misc feature

<222> (305)..(305)

<223> The 'Xaa' at location 305 stands for Arg, or Lys.

<400> 10

Met Val Lys Phe His Thr Leu Ser Val Ala Ile Leu Ala Ile Ala 10

Ser Ser Asn Thr Ile Phe Ala Thr Phe Arg Ser Asn Gly Lys Thr Phe

Gly Asp Glu Ser Val Ser Leu Leu Glu His Glu Ser Thr Ser Leu Ser

Arg Gly Pro Arg Pro Thr Glu Asp Gln Ile Ser Gln Leu Pro Lys Asn

Val Phe Phe Leu Leu Asp Asn Ser Ile Asp Met Ser Ile Glu Thr Gly 75

Glu Glu Asn Arg His Phe Leu Ser Glu Phe Phe Lys Leu Leu Lys Lys 90

Tyr Glu Gly Ile Asn Val Ser Leu Ile Arg Tyr Asn Ser Glu Glu Pro

Leu Gly Ser Thr Lys Ala Leu Thr Asn Gly Glu Leu Lys Lys Leu Ser 125 115 120

Asp Asn Ile Pro Thr Lys Met Pro Phe Asp Ile Gly Val Val Pro Thr 130

Gly Ile Gly Ala Ala Leu Lys Gln Ile Lys Thr Leu Tyr Pro Asp His 145 155 160

Glu Lys Phe Leu Val Gly Asn Thr Ile Thr Glu Leu Asp Tyr Ser Lys 165

Ala Leu Gly Lys Asp Ile Val Val Ile Val Phe Thr Thr Gly His Val 180

## WO 2005/026199 PCT/EP2004/052169 26/29

Ile	Asp	Pro 195	Tyr	Leu	Ala	Tyr	Asp 200	Glu	Ala	Phe	Asp	Ala 205	Arg	Arg	Asn
Gly	Val 210	Arg	Phe	Tyr	Val	Ile 215	Asn	Arg	Gly	Gly	Lys 220	Ala	Lys	Asn	Tyr
Trp 225	Thr	Gln	Leu	Leu	Gly 230	Cys	His	Tyr	Asn	Thr 235	Суз	Leu	Ser	Tyr	Ile 240
Arg	Ala	Lys	Ile	Thr 245	Arg	Pro	Ser	Leu	Tyr 250	Leu	Asp	Val	Leu	Val 255	Asn
Arg	Ile	Val	Ser 260	Lys	Arg	Ala	Lys	Asp 265	Ala	Val	Сув	Leu	Glu 270	Val	Trp
Thr	Asp	Tyr 275	Lys	Pro	Asn	Thr	Glu 280	Lys	Ser	Asp	Val	Arg 285	Ile	Met	Thr
Ser	Thr 290	Leu	Lys	Leu	Tyr	Lys 295	Thr	Leu	Leu	Thr	Gly 300	Ser	Phe	Ala	Glu
305	Asn		_	_	310		_	_		315		-	_		320
Lys	Arg	Gln	Ile	Phe 325	Cys	Tyr	Ser	Asn	Lys 330	Cys	Ala	Pro	Thr	Ile 335	Tyr
	Arg		340		_			345		_			350	-	-
	Lys	355			_		360		_			365			
	Val 370					375				-	380				
385	Gly			_	390					395					400
	Tyr			405					410				_	415	
	Glu	_	420		_		_	425					430		
inr	Val	vaı	vaı	Asp	Inr	Pro	GIU	ıyr	vaı	GIN	nys	val	Hls	Glu	Arg

445

22

24

Glu Met Gln Phe Asp Glu Glu Ser Thr His Leu Pro Asn Ser Gly Asn 450 455

440

His His Pro Pro His His Arg Lys Gly Ala Asn Gly Ser Gly Lys Lys 470

Thr Thr Ile Val Val Gly Ile Ile Cys Leu Val Val Ile Cys Ala Val 485

Ile Ala Gly Ala Tyr Leu Ser Leu Ser Gln Gln Glu Ser Val Glu Leu

Thr Ser Glu Glu Gly Asp Phe Leu Asn Asp Thr Thr Gly Gly Gln Pro

Glu Val Leu Glu Thr Gln Gln Val Val Asp Ala Glu Asn Lys Thr Trp 535

Leu 545

<210> 11

<211> 22

<212> DNA

<213> Artificial

435

<220>

<223> primer 1

<400> 11

ccacggctct ggaatctatg tc

<210> 12

<211> 24

<212> DNA <213> Artificial

<220>

<223> primer 2

<400> 12

caaaaggata cctatatttg gtac

<210> 13

<211> 27 <212> DNA <213> Artificial

<220>

28/29

<223>	Primer 3	
<400> tgtggt	13 agat gaatctgcta gtatatc	27
<210><211><211><212><213>	27	
<220> <223>	Primer 4	
	14 cacg gcattcagca acattta	27
	27	
<220> <223>	Primer 5	
	15 teca tgcagttaca taacaaa	27
<220>	27 DNA Artificial	
<400>	Primer 6  16  cttc tgagcaaagg aaatagg	27
<210><211><211><212><213>	27	
<220> <223>	Primer 7	
<400> cccgaat	17 Etcg tggtagatga atctgct	27
<220> <223>	Primer 8	

WO 2005/026199 PCT/EP2004/052169 29/29

<400> cccgtc	18 gact gcctcgcccc aaatgttgt	29
<210>	19	
<211>	30	
<212>		
<213>	Artificial	
-220		
<220>	Producer 0	
<223>	Primer 9	
<400>	19	
	ttcc atgatggtga agttccacac	30
<210>		
<211>		
<212>	DNA Artificial	
<213>	Aftificial	
<220>		
	Primer 10	
<400>	20	
cccgtc	gacg ttggcccct ttcggtgat	29